

FIG. 1

1 CCCTTCTCCAGGACTCTGGCTGCCAGCAGCTCCGCCCTTTTCAGATCAATTCTCGACCACC 60
 61 CACCTTGGGACTGCCGCCAGTCTCTGCCCTCTGGATCAGTGGGTCCAGACAGCCCCCT 120
 121 CCAGGACCTCAAAGCACCCCCGACCTAAGTCAACAGCCCACTGGCCCCCAGACGCAGTGG 180
 240 GCTCCGCTGACTCTCTTGGACACCTCCTGGGAGGAAATGCTCCCTGTCTGCCATCGTTT 240
 181 M L P V C H R F
 241 TTGCGACCACTCCTCCTCCTCTCTTGGTGGCTCGACGACCCCTGGCCCCCGCCAGC 300
 301 C D H L L L L L L L P S T T L A P A P A
 360 ATCCATGGGCCCCGCTGCCGCCCTGCTCCAGTTCTTGGGCTTCCCGAAGCGCCCCGGAG 360
 361 S M G P A A A L L Q V L G L P E A P R S
 420 CGTCCCCACACACCGACCTGTGCCTCCTGTCAATGTGGCGCCTATTCCGTGCGCGTGACCC 420
 480 V P T H R P V P P V M W R L F R R R D P
 481 CCAGGAGGCCAGAGTGGGACGCCCTCTGCGGCCATGCCACGTGGAGGAACTAGGGTCGC 480
 540 Q E A R V G R P L R P C H V E E L G V A
 541 CGGAAACATTGTGCGGCCACATCCCCGACAGCGGTCTGTCTCCTCCAGGCCCGCACACCCGC 540
 600 G N I V R H I P D S G L S S R P A Q P A
 541 CAGGACCTCGGGGCTGTGCCCCGAGTGGACAGTCGTCTTTGACCTGTGCGAATGTGGAGCC 600
 660 R T S G L C P E W T V V F D L S N V E P
 601 CACAGAGCGCCCCAACACGCGCGCTTAGAGTTGCGGCTGGAGGCTGAGTGTGAAGATAC 660
 T E R P T R A R L E L R L E A E C E D T

FIG. 2a

661 AGGAGGTGGGAGCTAAGCGTGGCACTGTGGGCGGACGACATCCAGGGCCTGAGCT 720
G G W E L S V A L W A D A E H P G P E L

721 GCTGGCGTGGCGGCGCACAGGGTGCTCCTGCGCGCAGACCTACTGGGGACTGCAGT 780
L R V P A P P G V L L R A D L L G T A V

781 AGCCGCCAACGCATCAGTGCCCTGTACTGTGCGCCTGGCGCTGTCACTGCACCCTGGGCG 840
A A N A S V P C T V R L A L S L H P G A

841 CACTGCAGCCTGTGGGCGCCTGGCTGAGGCCTCCCTGCTGCTGGTGACGCTGGACCCACG 900
T A A C G R L A E A S L L L V T L D P R

901 CCTGTGCCCTTGCCGCGATTGGCGGCGCACACGAGGCCAGGGTAGAAGTTGGTCCAGT 960
L C P L P R L R R H T E P R V E V G P V

961 GGGCACTTGTCGTACCCGACGGTTGCATGTGAGCTTCCGTGAGGTGGGCTGGCACCGTTG 1020
G T C R T R R L H V S F R E V G W H R W

1021 GGTGATCGGCGCGTGGCTTCCTAGCCAACTTCTGCCAGGCGACGTGCGCACTACCCGA 1080
V I A P R G F L A N F C Q G T C A L P E

1081 AACGCTAGGGGACCCGGCGGCGCCTGCACTCAACCACGCTGTGCTGCGCGCGCTCAT 1140
T L R G P G G P P A L N H A V L R A L M

1141 GCACGCAGCTGCTCCACCCCGGTGCAGGCTCGCCCTGCTGCGTCCAGAGCGTCTATC 1200
H A A A P T P G A G S P C C V P E R L S

1201 ACCCATCTCCGTGCTCTTCTCGACAATAGTGACAACGTGGTCTCGACACTACGAAGA 1260
P I S V L F F D N S D N V V L R H Y E D

1261 CATGGTGGTGATGAGTGTGGTGCCGTTGACCACCCGGGACACCCCTTTCAGGGACCGCC 1320
M V V D E C G C R

1321 CCACGCAAAAGCAGGACTGTTGTTTCATGTTTATTGGTGACAAAAGCTTAAACAAA 1380

1381 TTGACT 1387

FIG. 2b

GDF-1 RRHTEPRVEVG--PVGTORTRRLHVSE-REVGWHRWVIAPRGFLANFQGTALPETLRPGGPP
 Vg-1 RKRSYSKLPFT--ASNIKKRRLHYVEF-KDVGWQNWVIAPOGYMANYCYGEP-YPLTEILNG--
 Vgr-1 GSGSSDYNGSE--LKTAKKKHELHYVSE-QDLGWQDWIIAPKGYAANYCDGEC-SFPLNAHMNA--
 BMP-2a KROAKHKQRR--LKSSKKRHPLYVDF-SDVGWNDWIVAPPGYHAFYCHGEC-P-FPLADHLNS--
 BMP-2b SPKHHSORARK--KNKNRRRHSLYVDF-SDVGWNDWIVAPPGYQAFYCHGEC-P-FPLADHLNS--
 BMP-3 TLKKARRKQWI--EPRNRRRHSLYVDF-ADIGWSEWII SPKSFDAYYCHGEC-P-FPMPKSLKPS--
 DPP -HARRPTRRKN--HDDTARRHSLYVDF-SDVGWDDWIVAPLGYDAYYCHGEC-P-FPLADHENS--
 MIS GRAQRSAGATA--ADGPARREL SVDLRAE----RSVLIPETIYOANNCHGEC-PGWQSDRNPRY--
 Inhibin α RLLQRPPEEPA--AHANRRVALNISE-OELGWERWIVYPPSEIFHYCHGEC-PGLHIPNLSLPV-
 Inhibin β GLE---CDGKV---NLC--KKQEFFVSE-KDIGWNDWIIAPSGYHANYCHGEC-PSHIAGTSGSSL-
 Inhibin β GLE---CDGRT---NLC--RQOEFIDE-RLIGWNDWIIAPTGYGNYCHGEC-PAYLAGVPGSAS-
 TGF- β 1 ALDTNYCFSSST--EKNCLVRQ--LYIDFRKDLGWK-WIHEPKGYHANFCHGEC-PYIW---SLD-
 TGF- β 2 ALDAAYCFERNV--QDNCVLRP--LYIDFRKDLGWK-WIHEPKGYNANFCHGEC-PYIW---SSD-
 TGF- β 3 ALDTNYCFERNL--EENCVVRP--LYIDFRQDLGWK-WVHEPKGYANFCHGEC-PYLR---SAD-
 TGF- β 4 DLDTDYCFGPGTDEKNCVVRP--LYIDFRKDLQWK-WIHEPKGYMANFCHGEC-PYIW---SAD-
 TGF- β 5 GVGQEYCFGNN--GPNCVVKP--LYINFRKDLGWK-WIHEPKGYEANYCHGEC-PYIW---SMD-

FIG. 3a

GDF-1	ALNHAVLRALMHAAA-PTPGAGSPCCV--PERLSPISVLFF-DNSDNNVLRHYEDMVVDE	CR
Vg-1	--SNHAILOTLVHS--IEPEDIPLPCQV--PTKMSPISMLFY-DNNDNNVLRHYENMAVDE	CR
Vgr-1	--TNHAIIVQTLVHL--MNPEYVPKPCQA--PTKLNIAISVLVF-DDNSNVILKKYRNMVVR	CR
BMP-2a	--TNHAIIVQTLVNS--VNSKIPKACQV--PTELSAISMLYL-DENEKVVLNKYQDMVVEG	CR
BMP-2b	--TNHAIIVQTLVNS--VNSSIPKACQV--PTELSAISMLYL-DEYDKVVLNKYQEMVVEG	CR
BMP-3	--NHATIOQISIVRA-VGVVPGIPEPCQV--PEKMSSAISLFF-DENKNNVILKVYPNMTVES	CR
DPP	--TNHAVVQTLVNN--MNPQKVPKACQV--PTQLDSVAMLYLND-QSTVVLNKYQEMTVVG	CR
MIS	--GNH-VVLLL-KMQARGAALARPPCQV--PTAYAGKLLISLSEER--ISAHVPNNMVATE	CR
Inhibin α	--PGAPPT---PAQPYSLPLGAQPCQAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQH	CR
Inhibin β A	--SFHSTVINHYRMRGHSPEANLKSQCV--PTKLRPMSMLYY-DDGQNIKKDIONMIVEE	CR
Inhibin β B	--SFHTAVVNQYRMRLNPGT-VNSQCV--PTKLSMTSMMLYF-DDEYNIVKRDVPNMIVEE	CR
Inhibin β C	--TOYSKVLALYN--QHNPGASAAPCQV--PQALEPLPIVYY-VGRKPKV-EQLSNMIVRS	CR
TGF- β 1	--TQHSRVLSLYN--TINPEASASPCQV--SQDLEPLTILYY-IGKTPKI-EQLSNMIVKS	CR
TGF- β 2	--TTHSTVLGLYN--TLNPEASASPCQV--PQDLEPLTILYY-VGRTPKV-EQLSNMVVKS	CR
TGF- β 3	--TOYTKVLALYN--QHNPGASAAPCQV--PQTLDPPIIYY-VGRNVRV-EQLSNMVVR	CR
TGF- β 4	--TOYSKVLALYN--QNNPGASISPCQV--PDVLEPLPIIYY-VGRTAKV-EQLSNMVVRS	CR
TGF- β 5	--TOYSKVLALYN--QNNPGASISPCQV--PDVLEPLPIIYY-VGRTAKV-EQLSNMVVRS	CR

FIG. 3a CONT!

	GDF-1	Vg-1	Vgr-1	BMP-2a	BMP-2b	BMP-3	DPP	MIS	Inhibin α	Inhibin βA	Inhibin βB	TGF- $\beta 1$	TGF- $\beta 2$	TGF- $\beta 3$	TGF- $\beta 4$	TGF- $\beta 5$
GDF-1	100	52	40	38	39	41	34	33	22	31	31	26	27	30	26	26
Vg-1	-	100	59	59	57	45	49	27	23	45	40	34	35	38	33	35
Vgr-1	-	-	100	62	59	43	57	26	23	45	39	35	37	38	37	37
BMP-2a	-	-	-	100	92	44	73	26	20	42	37	34	34	35	33	33
BMP-2b	-	-	-	-	100	44	74	27	21	41	37	33	34	35	33	33
BMP-3	-	-	-	-	-	100	42	25	28	33	33	29	31	31	26	28
DPP	-	-	-	-	-	-	100	25	20	39	36	35	35	35	35	34
MIS	-	-	-	-	-	-	-	100	18	22	22	24	21	26	25	24
Inhibin α	-	-	-	-	-	-	-	-	100	23	21	24	23	24	24	24
Inhibin βA	-	-	-	-	-	-	-	-	-	100	63	38	37	36	35	38
Inhibin βB	-	-	-	-	-	-	-	-	-	-	100	35	35	36	34	32
TGF- $\beta 1$	-	-	-	-	-	-	-	-	-	-	-	100	73	77	85	81
TGF- $\beta 2$	-	-	-	-	-	-	-	-	-	-	-	-	100	81	68	69
TGF- $\beta 3$	-	-	-	-	-	-	-	-	-	-	-	-	-	100	74	73
TGF- $\beta 4$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	78
TGF- $\beta 5$	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100

FIG. 3b

133 T - 124

54

GDF-1

PVPPVMWRLFRRRDPQEARVGRPLRPPCHVEELGVAGNIVRHIPDSGLSSKFAQFARISGCELEWIVVIDSERVF
IIII IIII I I III I

DUMSIUWTBIENORMCGSSIOKKKPDLCFEVEFNVPGSVIRFPDQGRIIPYSDDIHPTQCLEKRLFFNFISAIEKEERV

vq-1

46

234

219

GDF-1 SLLLVTLDPRLCPLPR

SUBJECT:

Va-1 SLLTVTLNPLRCKRPR

243

228

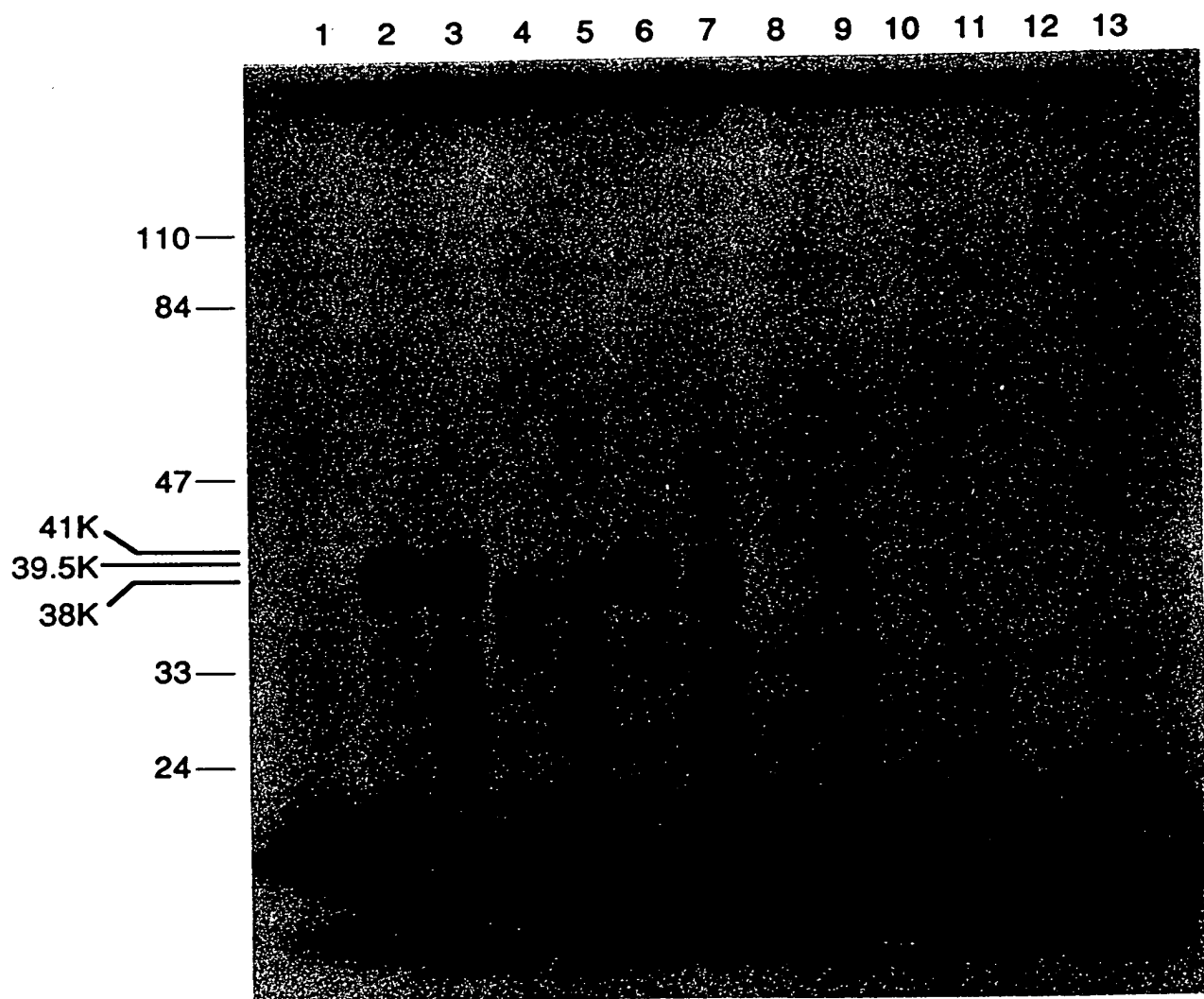


FIG. 4

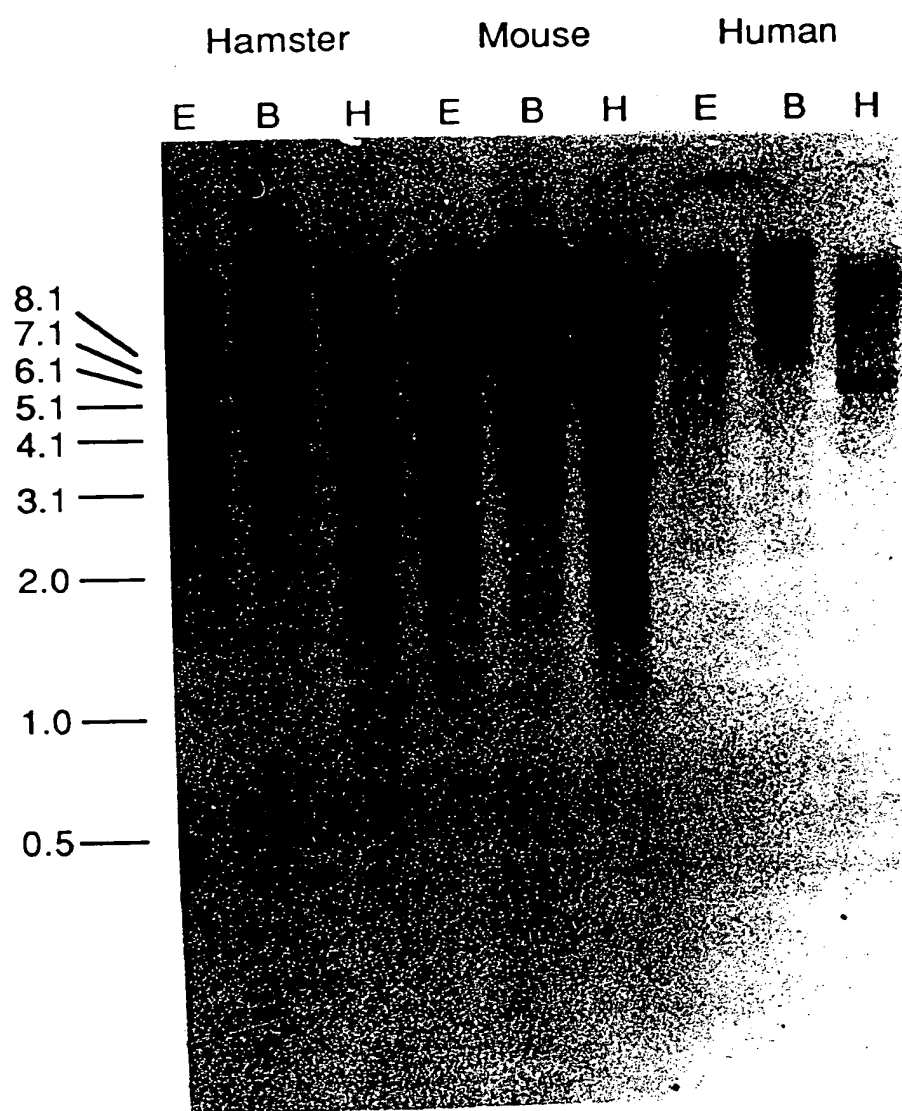


FIG. 5

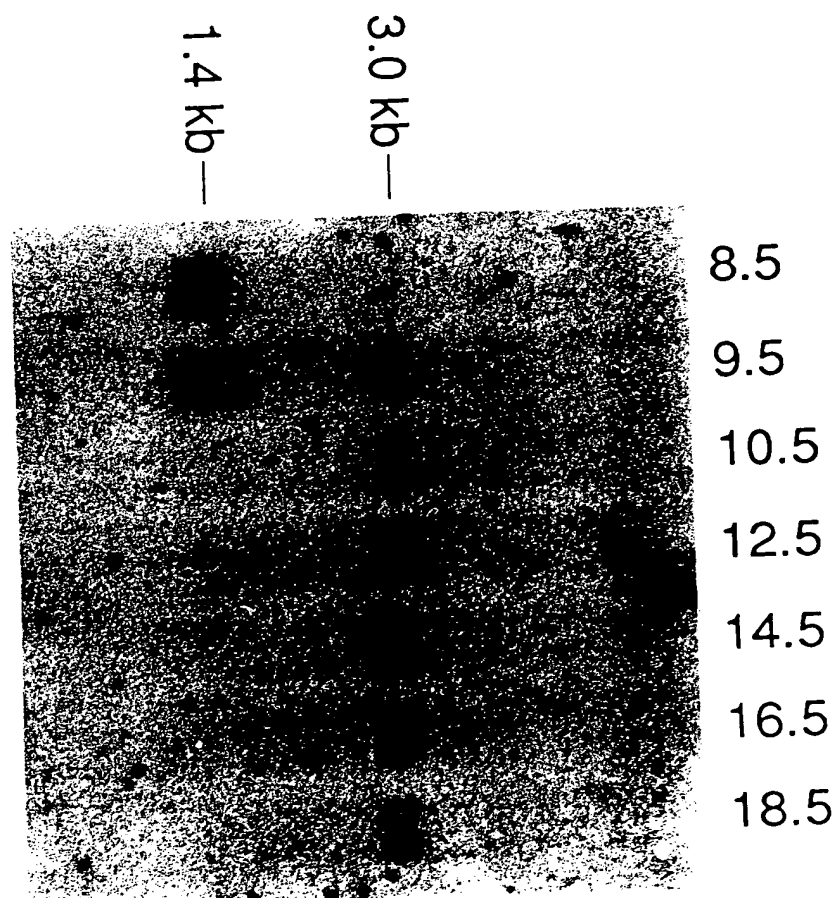
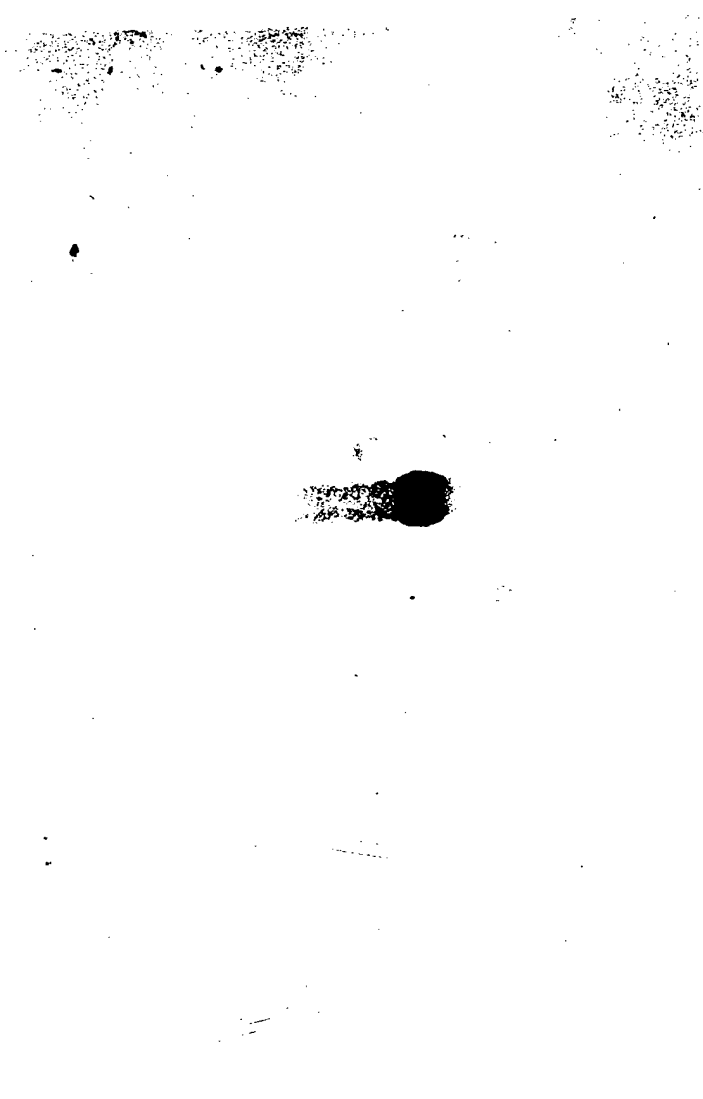


FIG. 6

3.0 kb -



10.5 d placenta
testis
seminal vesicle
ovary
oviduct
uterus
brain
thymus
heart
lung
kidney
adrenal
spleen
liver
intestine
pancreas

FIG. 7

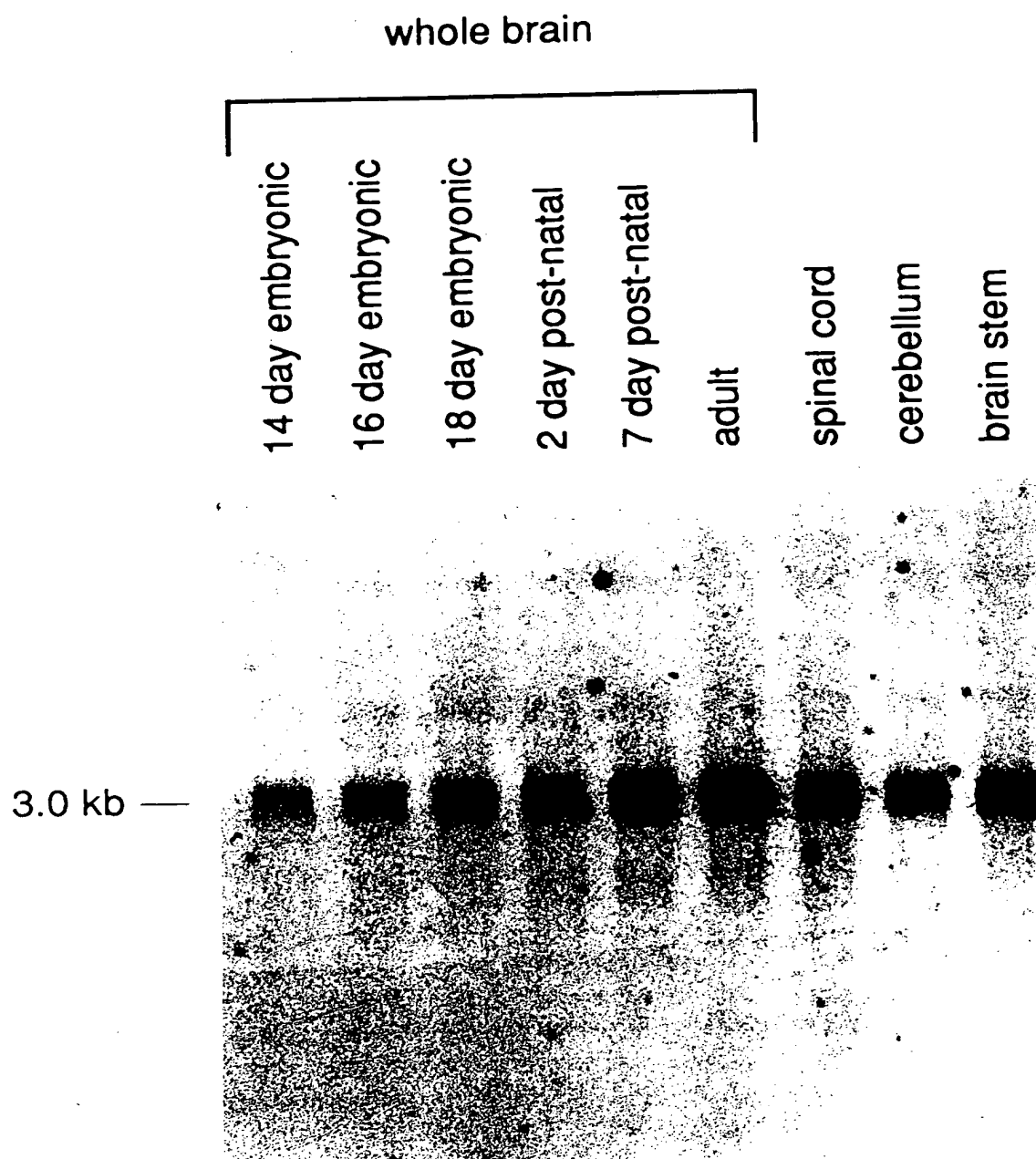


FIG. 8

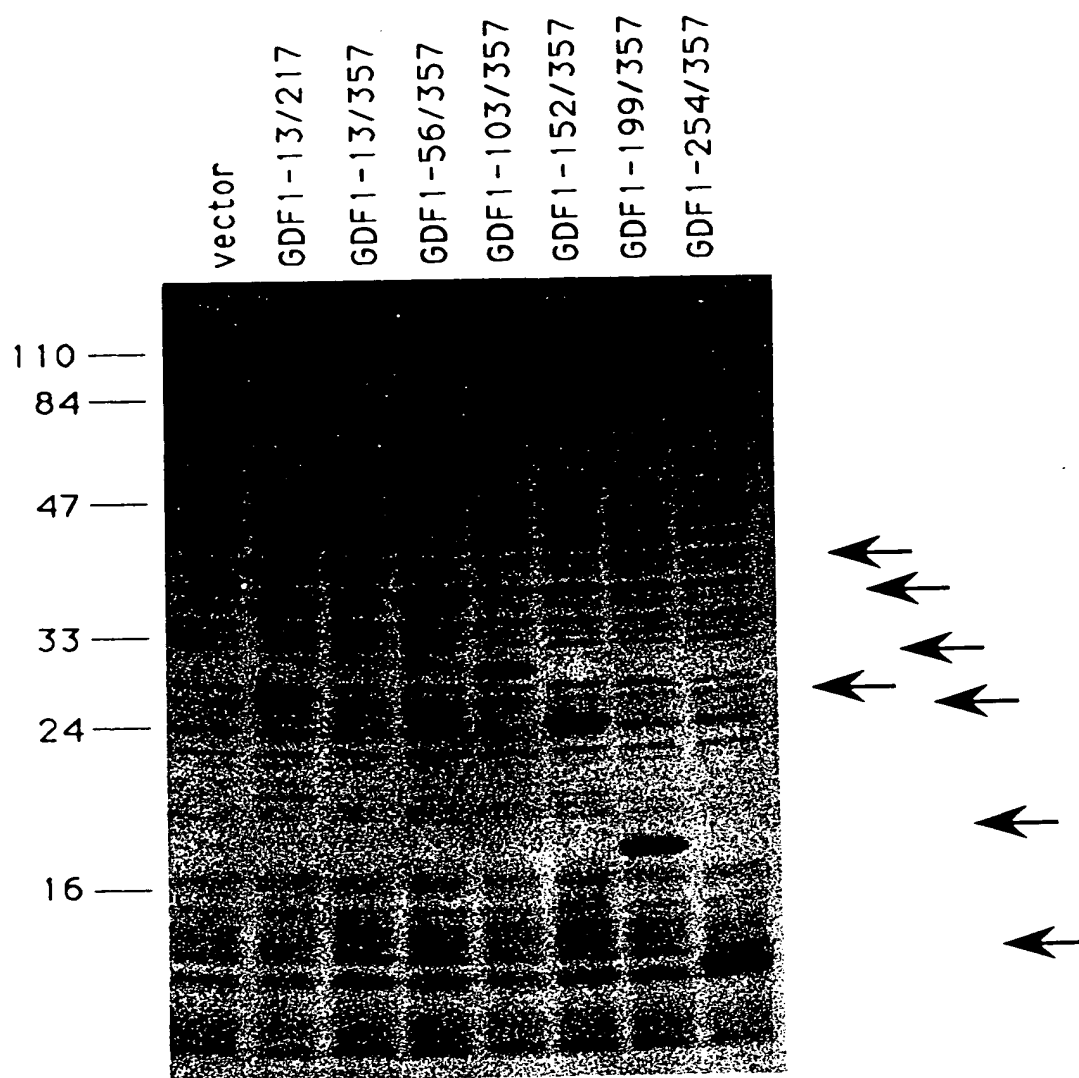
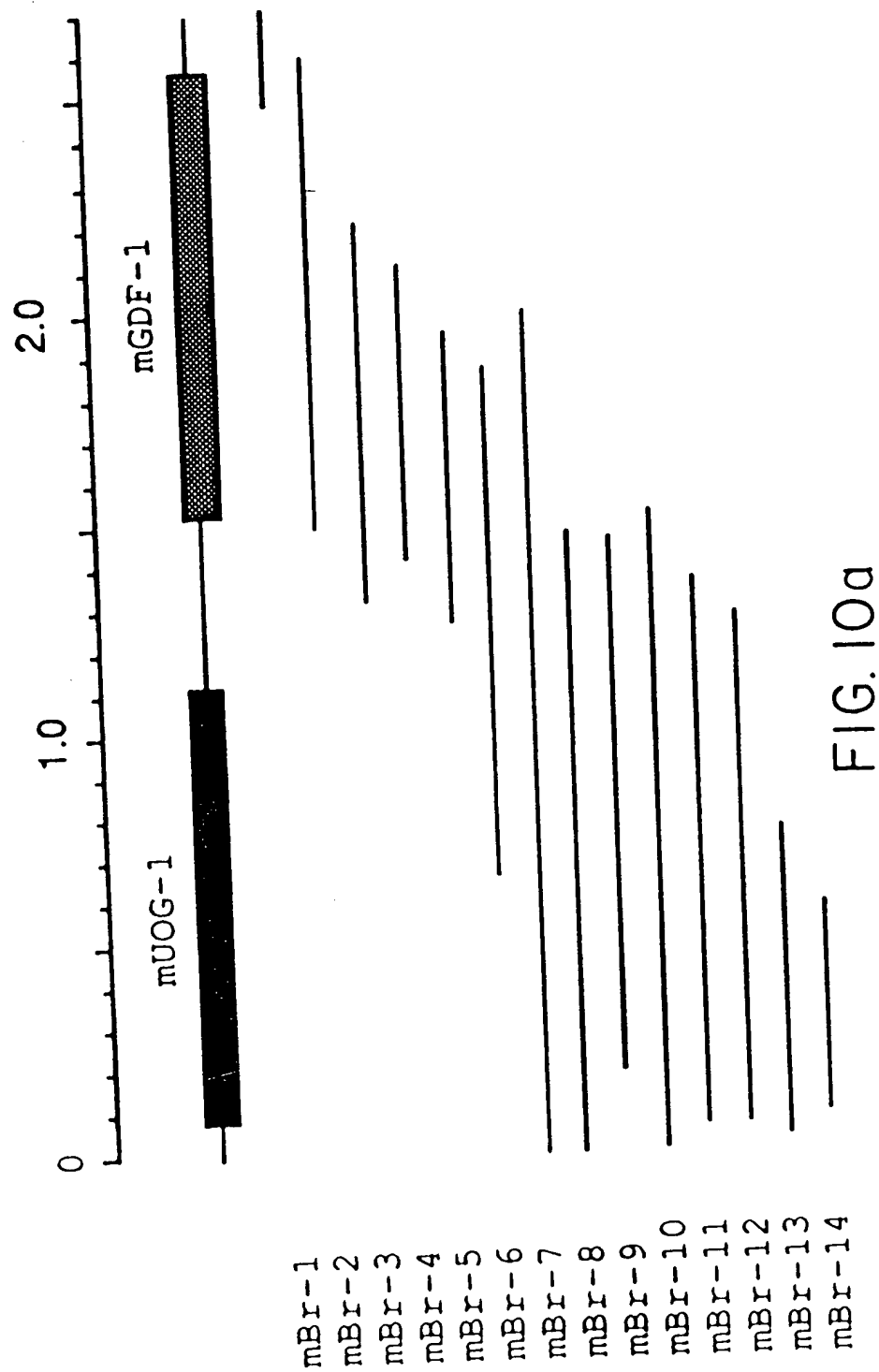


FIG. 9



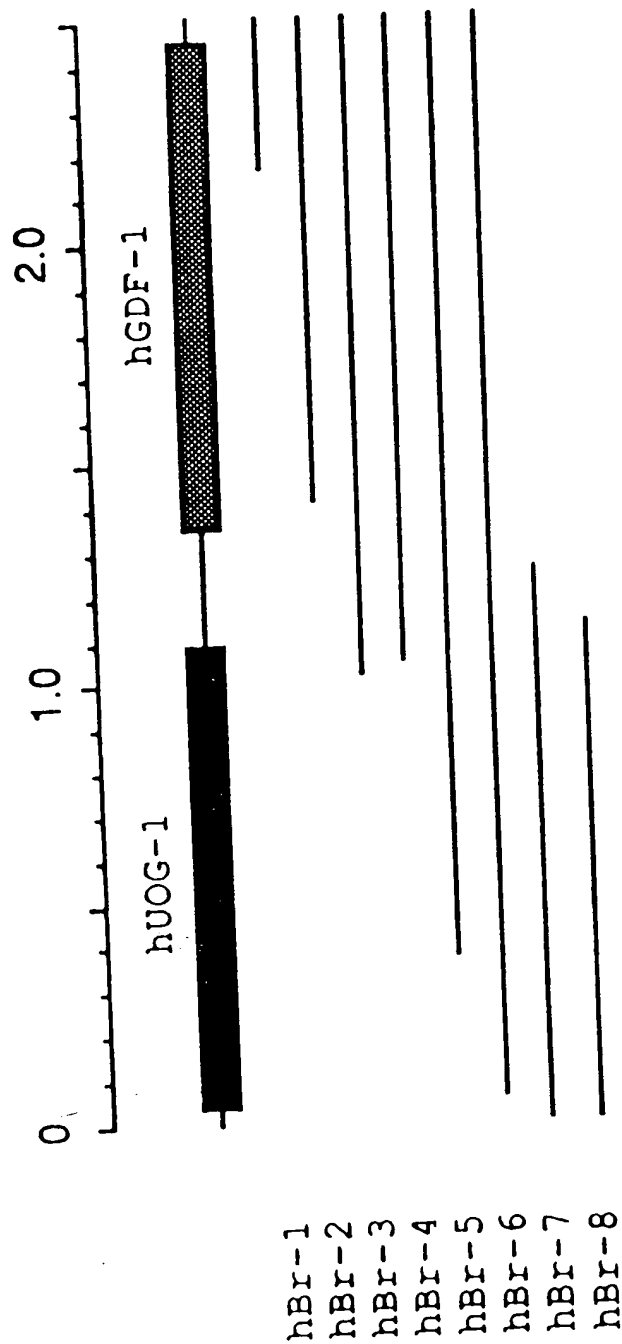


FIG. 10b

1	GCGCGTGACGCGAGGGCGCGCGGCGACTCGGACCGGTGCAGGCAACA	60
61	AGAATTGGATAGCATGGCTGCTGCCGCGGCGACCCCAAGGCTCGAGGCGCCAGAGCCCAT	120
	M A A A A A A T P R L E A P E P M	
121	GCCGAGTTATGCGCAGATGTTGCAACGAAGCTGGGCCTCGGCGCTGGCGGCGGCTCAGGG	180
	P S Y A Q M L Q R S W A S A L A A A Q G	
181	CTGCGGGGACTGCGGCTGGGGACTGGCGCGCGCGGCTGGCGGAGCACGCGCACCTGGC	240
	C G D C G W G L A R R G L A E H A H L A	
241	TGCACCGAGCTGCTGCTGGCCGTGCTCTGCGCTCTGGGGTGGACAGCGTTGCGCTGGGC	300
	A P E L L L A V L C A L G W T A L R W A	
301	AGCCACCACACACATCTTTCGGCCCCCTGGCCAAGCGGTGTCGTCTGCAGCCTAGAGATGC	360
	A T T H I F R P L A K R C R L Q P R D A	
361	TGCCAGGTTACCTGAGAGCGCCTGGAAGCTTCTGTTCTACTTGGCCTGTTGGAGCTACTG	420
	A R L P E S A W K L L F Y L A C W S Y C	
421	CGCTTACCTGCTCCTGGGCACCAAGTTATCCTTTCTTCCATGACCCGCCCTCTGTCTTCTA	480
	A Y L L L G T S Y P F F H D P P S V F Y	
481	TGACTGGAGGTCAGGCATGGCAGTGGCCTGGGACATCGCGGTGGCCTATTGCTGCAGGG	540
	D W R S G M A V P W D I A V A Y L L Q G	
541	GAGTTTCTACTGCCACTCCATCTATGCCACCGTGTACATGGACAGCTGGCGTAAGGACTC	600
	S F Y C H S I Y A T V Y M D S W R K D S	
601	GGTGGTCATGCTGGTGCATCACGTGGTCACCCCTGCTCCTCATTGCCTCTTCTACGCCCT	660
	V V M L V H H V V T L L L I A S S Y A F	
661	CCGGTACCACAACGTAGGCCTCCTCGTGTCTTCTTCTGTCATGACGTACGCGATGTGCAGCT	720
	R Y H N V G L L V F F L H D V S D V Q L	
721	GGAGTTACAAAACTCAACATCTACTTTAAGGCTAGGGGTGGTGCCTACCATCGCTTGCA	780
	E F T K L N I Y F K A R G G A Y H R L H	
781	TGGGCTGGTGGCCAACCTGGGCTGCCTCAGCTTCTGTTTCTGCTGGTTCTGGTTCCGCCT	840
	G L V A N L G C L S F C F C W F W F R L	
841	CTACTGGTTCCCGCTCAAGGTTCTGTACGCCACTTGCCACTGCAGCCTGCAGTCTGTGCC	900
	Y W F P L K V L Y A T C H C S L Q S V P	
901	TGACATTCCGTACTACTTCTTCTTCAACATTCTGCTGTTGCTCCTGATGGTCATGAACAT	960
	D I P Y Y F F F N I L L L L M V M N I	
961	CTATTGGTTCTGTACATTGTGGCTTTCGCAGCCAAGGTGCTGACTGGTCAGATGCGTGA	1020
	Y W F L Y I V A F A A K V L T G Q M R E	
1021	ACTGGAAGACTTGAGGGAGTACGACACTCTGGAAGCTCAGACAGCCAAGCCCTGCAAAGC	1080
	L E D L R E Y D T L E A Q T A K P C K A	
1081	CGAGAAGCCACTGAGGAATGGCCTGGTGAAGGACAAGCTCTTCTGAGTCTCTTGCTCCTCA	1140
	E K P L R N G L V K D K L F	
1141	ACTTCAGCCATCCAGGACTCTATCCCATCCTACCTGGGATACTGACTCCGCCCCCTGGAGA	1200
1201	CTCGACCCAGTCCCTGGAGGTCTGCTCCACCCCTGGAGGCCCCGTCCCGCCTTTGGCGG	1260
1261	CATGGCCTCGCCCCCTAGGACAATAGCCCCGCCCTAAGATTGAGGATGCTACCCCTTCTCCA	1320
1321	GGGACTCTGGCTGCCAGCAGCTCCGCCTTTTCAGATCAATTCTCGACCAACCCACCTTGGGA	1380
1381	CTGCGCGCCAGTCCCTGCCCTCTGGATCAGTGGGGTCCAGACACGCCCCCTCCAGGACCTC	1440
1441	AAAGCACCCCCGACCTAAGGTCACGACCCCACTGGCCCCAGACGAGTGGGCTCCGCTGA	1500
1501	CTCTCTTGGACACCTCCTGGGAGGAAAATGCTCCCTGTCTGCCATCGTTTTTTCGACCAC	1560
	M L P V C H R F C D H	

FIG. 11a

1561	CTCCTCCTCCTGCTCTTGCTGCCCTCGACGACCCTGGCCCCCGGCCAGCATCCATGGGC	1620
	L L L L L L L P S T T L A P A P A S M G	
1621	CCCGCTGCCGCCCTGCTCCAGGTTCTTGGGCTTCCCGAAGCGCCCGGAGCGTCCCCACA	1680
	P A A A L L Q V L G L P E A P R S V P T	
1681	CACCGACCTGTGCCTCCTGTCATGTGGCGCCTATTCCGTCGCCGCGACCCCCAGGAGGCC	1740
	H R P V P P V M W R L F R R R D P Q E A	
1741	AGAGTGGGACGCCCTCTGCGGCCATGCCACGTGGAGGAAGTAGGGGTGCGCGAAACATT	1800
	R V G R P L R P C H V E E L G V A G N I	
1801	GTGCGCCACATCCCCGACAGCGTCTGTCTCCAGGCCCCGACAACCCGCCAGGACCTCG	1860
	V R H I P D S G L S S R P A Q P A R T S	
1861	GGGCTGTGCCCCGAGTGGACAGTCGTCTTGACCTGTGCAATGTGGAGCCACAGAGCGC	1920
	G L C P E W T V V F D L S N V E P T E R	
1921	CCAACACGCGCGCGCTTAGAGTTGCGGCTGGAGGCTGAGAGTGAAGATACAGGGGGTGG	1980
	P T R A R L E L R L E A E S E D T G G W	
1981	GAGCTAAGCGTGGCACTGTGGGCGGACGCAGAGCATCCAGGGCCTGAGCTGCTGCGCGTG	2040
	E L S V A L W A D A E H P G P E L L R V	
2041	CCGCGCCACCAGGGGTGCTCCTGCGCGCAGACCTACTGGGGAAGTGCAGTAGCCGCAAC	2100
	P A P P G V L L R A D L L G T A V A A N	
2101	GCATCAGTGCCTGTACTGTGCGCCTGGCGCTGTCACTGCACCCTGGGGCCACTGCAGCC	2160
	A S V P C T V R L A L S L H P G A T A A	
2161	TGTGGGCGCCTGGCTGAGGCCTCCCTGCTGCTGGTGACGCTGGACCCACGCCTGTGTCCC	2220
	C G R L A E A S L L L V T L D P R L C P	
2221	TTGCCGCGATTGCGGCGCCACACGGAGCCCAGGGTAGAAGTTGGTCCAGTGGGCACTTGT	2280
	L P R L R R H T E P R V E V G P V G T C	
2281	CGTACCCGACGGTTGCATGTGAGCTTCCGTGAGGTGGGCTGGCACCGTTGGGTGATCGCG	2340
	R T R R L H V S F R E V G W H R W V I A	
2341	CCGCGTGGCTTCCCTAGCCAACCTTCTGCCAGGGCACGTGCGCACTACCCGAAACGCTGAGG	2400
	P R G F L A N F C Q G T C A L P E T L R	
2401	GGACCCGGCGGGCCGCTGCACTCAACCACGCTGTGCTGCGCGCGCTCATGCACGCAGCT	2460
	G P G G P P A L N H A V L R A L M H A A	
2461	GCTCCCACCCCGGGTGCAGGCTCGCCCTGCTGCGTGCCAGAGCGTCTATCACCCATCTCC	2520
	A P T P G A G S P C C V P E R L S P I S	
2521	GTGCTCTTCTTCGACAATAGTGACAACGTGGTCTGCGACACTACGAAGACATGGTGGTG	2580
	V L F F D N S D N V V L R H Y E D M V V	
2581	GATGAGTGTGGCTGCCGTTGACCACCCGGGACACCCTTTCAGGGACCGCCCCACGCAAAA	2640
	D E C G C R	
2641	GCAGGGACTGTTTGTTCATGTTTTATTGGTGACAAAAAGCTTAAAACAAATTTGACTAAA	2700
2701	AATTAAGTTCC 2711	

FIG. 11a CONT.'

1	GGACACGGCGGGCGAGCGGGCGGTATGGCGGGCGGGGGCCCGCGGCGGGGCGGACGGGG	60
	M A A A G P A A G P T G	
61	CCCAGACCCATGCCGAGCTACGCGCAGCTAGTGCAGCGCGGCTGGGGCAGCGCGCTGGCG	120
	P E P M P S Y A Q L V Q R G W G S A L A	
121	GCGGCGCGGGGCTGCACGGAAGTGCAGCGGCTGGGGGCTGGCGCGTTCGCGGCTGGCTGAGCAC	180
	A A R G C T D C G W G L A R R G L A E H	
181	GCGACCTGGCGCGCGGCGGAGCTGCTGCTGGCGCTGGCGCGCTGGGCTGGACCGCG	240
	A H L A P P E L L L L A L G A L G W T A	
241	CTGCGCTCCGCGGCACTGCGCGCTCTTTCGGCCCCCTGGCGAAGCGGTGCTGCCTCCAG	300
	L R S A A T A R L F R P L A K R C C L Q	
301	CCCAGAGATGCCGCCAAGATGCCCGAGAGCGCTTGAAGTTTCTTCTTCTACCTGGGCAGC	360
	P R D A A K M P E S A W K F L F Y L G S	
361	TGGAGCTACAGTGCTACCTGCTGTTTGGCACCAGTACCCCTTCTTCCATGACCCACCA	420
	W S Y S A Y L L F G T D Y P F F H D P P	
421	TCTGTCTTCTACGACTGGACGCCGGGCGATGGCAGTGCCACGGGACATTGCAGCCGCTAC	480
	S V F Y D W T P G M A V P R D I A A A Y	
481	CTGCTCCAGGAAGCTTCTATGGCCACTCCATCTACGCTACGCTATACATGGACACCTGG	540
	L L Q G S F Y G H S I Y A T L Y M D T W	
541	CGCAAGGACTCGGTGGTCATGCTGCTCCACCACGTGGTCACTCTCATCCTCATCGTCTCC	600
	R K D S V V M L L H H V V T L I L I V S	
601	TCCTACGCCTTCCGGTACCACAATGTGGGCATCCTTGTGCTCTTCTGCACGATATCAGT	660
	S Y A F R Y H N V G I L V L F L H D I S	
661	GACGTGCAGCTTGAGTTCACCAAGCTCAACATTTACTTCAAGTCCCGCGGGCGGCTCCTAC	720
	D V Q L E F T K L N I Y F K S R G G S Y	
721	CATCGGCTGCATGCCTTGGCAGCAGACTTGGGCTGCCTCAGCTTCGGCTTCAGCTGGTTC	780
	H R L H A L A A D L G C L S F G F S W F	
781	TGGTTCCGCCTTACTGTTTCCCGCTCAAGGTCTGTATGCCACCAAGTCACTGCAGTCTG	840
	W F R L Y W F P L K V L Y A T S H C S L	
841	CGCACGGTGCCTGACATCCCCTTCTACTTCTTCTTCAATGCGCTCCTGCTGCTGCTCACC	900
	R T V P D I P F Y F F F N A L L L L L T	
901	CTTATGAACCTTACTGGTTCTGTACATCGTGGCGTTTGCAGCCAAGGTGTTGACAGGC	960
	L M N L Y W F L Y I V A F A A K V L T G	
961	CAGGTGCACGAGCTGAAGGACCTGCGGGAGTATGACACAGCCGAGGCCAGAGCCTGAAG	1020
	Q V H E L K D L R E Y D T A E A Q S L K	
1021	CCCAGCAAAGCCGAGAAGCCACTGAGGAACGGCCTGGTGAAGGACAAGCGCTTCTGAACC	1080
	P S K A E K P L R N G L V K D K R F	
1081	CCTCGGCCCCGCCCCCGTGACCCGCCCCACCCGAATACCCCGGCCACGCTCCCCGTC	1140
	M P P P Q Q G P C G H H	
1141	CTTGGCCGCCCCCTCCACCCCTCCAACTCTGCTCCTCTAGGGCCGCGCCACCTCCCTG	1200
1201	GGACCCCGCCCCCTCATCCTGCCTCCATTTCCCGGCCACGCCCCCAGGACCCCTGCCCC	1260
1261	TCCGGGGACACCGCCCCGCTCAGCCCACTGGTCCCGGGCCGCGCGGACCTGCGCA	1320
1321	CTCTCTGGTTCATCGCTGGGAGGAAGATGCCACCGCCGAGCAAGGTCCCTGCGGCCACC	1380

FIG. 11b

1381 ACCTCCTCCTCCTCCTGGCCCTGCTGCTGCCCTCGCTG⁻CCC⁻TGACCCGCGCCCCCGTGC 1440
 L L L L L A L L L P S L P L T R A P V P
 1441 CCCCAGGCCAGCCGCGCCCTGCTCCAGGCTCTAGGACTGCGGATGAGCCCCAGGGTG 1500
 P G P A A A L L Q A L G L R D E P Q G A
 1501 CCCCAGGCTCCGGCCGGTCCCCCGGTCATGTGGCGCCTGTTTCGACGCGGGACCCCC 1560
 P R L R P V P P V M W R L F R R R D P Q
 1561 AGGAGACCAGGTCTGGCTCGCGGCGGACGTCCCCAGGGGTACCCCTGCAACCGTGCCACG 1620
 E T R S G S R R T S P G V T L Q P C H V
 1621 TGGAGGAGCTGGGGGTGCGCGGAAACATCGTGCGCCACATCCCGGACCGCGGTGCGCCCA 1680
 E E L G V A G N I V R H I P D R G A P T
 1681 CCGGGCCTCGGAGCCTGTCTCGGCCGCGGGCATTGCCCTGAGTGGACAGTCGTCTTCG 1740
 R A S E P V S A A G H C P E W T V V F D
 1741 ACCTGTGCGGCTGTGGAACCCGCTGAGCGCCCCGAGCCGGGCGCCCTGGAGCTGCGTTTCG 1800
 L S A V E P A E R P S R A R L E L R F A
 1801 CGGCGGCGGCGGCGGAGCCCGGAGGGCGGCTGGGAGCTGAGCGTGCGCAAGCGGGCC 1860
 A A A A A A P E G G W E L S V A Q A G Q
 1861 AGGGCGGCGGCGGAGCCCGGGCGGTGCTGCTCCGCCAGTTGGTGCCCGCCCTGGGGC 1920
 G A G A D P G P V L L R Q L V P A L G P
 1921 CGCCAGTGCGCGCGGAGCTGTGGGCGCGCCTTGGGCTCGCAACGCCTCATGGCCGCGCA 1980
 P V R A E L L G A A W A R N A S W P R S
 1981 GCCTCCGCCTGGCGCTGGCGCTACGCCCCGGGCCCCCTGCCGCTGCGCGCGCCTGGCCG 2040
 L R L A L A L R P R A P A A C A R L A E
 2041 AGGCCTCGCTGCTGCTGGTGACCCTCGACCCGCGCCTGTGCCACCCCTGGCCCGGCCGC 2100
 A S L L L V T L D P R L C H P L A R P R
 2101 GGCGCGACGCCGAACCCGTGTTGGGCGGCGCCCCGGGGGCGCTTGTGCGCGCGGGCGGC 2160
 R D A E P V L G G G P G G A C R A R R L
 2161 TGTACGTGAGCTTCCGCGAGGTGGGCTGGCACCCTGGGTCTATCGCGCCGCGCGGCTTCC 2220
 Y V S F R E V G W H R W V I A P R G F L
 2221 TGGCCAACTACTGCCAGGGTCAGTGCGCGCTGCCCGTCGCGCTGTGCGGGTCCGGGGGGC 2280
 A N Y C Q G Q C A L P V A L S G S G G P
 2281 CGCCGGCGCTCAACCACGCTGTGCTGCGCGCGCTCATGCACGCGGCCGCCCGGGAGCCG 2340
 P A L N H A V L R A L M H A A A P G A A
 2341 CCGACCTGCCCTGCTGCGTGCCCGCGCGCCTGTGCGCCATCTCCGTGCTCTTCTTTGACA 2400
 D L P C C V P A R L S P I S V L F F D N
 2401 ACAGCGACAACGTGGTGCTGCGGCAGTATGAGGACATGGTGGTGGACGAGTGCGGCTGCC 2460
 S D N V V L R Q Y E D M V V D E C G C R
 2461 GCTAACCCGGGGCGGGCAGGGACGCGGGCCCAACAATAATGCCGCGTGG 2510

FIG. 11b CONT.'

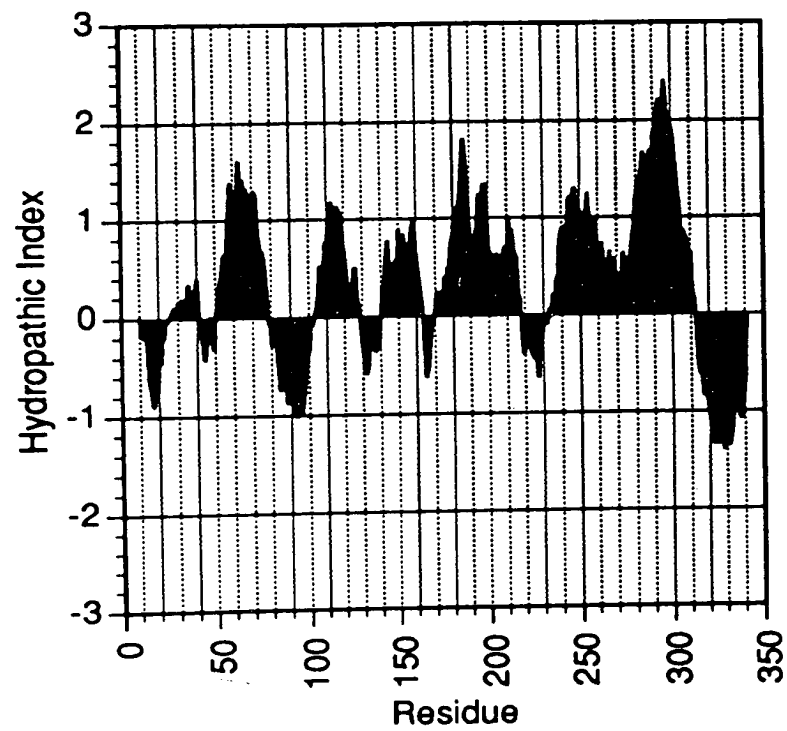


FIG. 12

167
 mGDF-1 ELLRVPAPP-GVLLRADLLGTAVAANASVPCTVRLALSLHPGATAACGRLAESLLLVTL 225
 hGDF-1 VLLRQLVPALGPPVRAELLGAAWARNASWPRSLRLALALRPRAPAACARLAESLLLVTL 240
 181
 226
 mGDF-1 DPRLC-PLPRIRRHTEPRVEVGPVGTPTRRRLHVSFREVGVHRWVIAPRGFLANFQQGTQ 284
 hGDF-1 DPRLCHPLARPRDAEPVLGGPGGAPRARRLYVSFREVGVHRWVIAPRGFLANYQQGQ 300
 241
 285
 mGDF-1 ALPETLRGPGGPPALNHAVLRALMHAAAPTPGAGSPCCVPERLSPISVLFFDSDNVVLR 344
 hGDF-1 ALPVALSGSGGPPALNHAVLRALMHAAAPGA-ADLPCCVPARLSPISVLFFDSDNVVLR 359
 301
 345
 mGDF-1 HYEDMVVDECGR 357
 hGDF-1 QYEDMVVDECGR 372
 360

FIG. 13a cont.

		60
	1	
mUOG-1	MAAAATPRLEAEPMP SYAQM LQRSWASALAAQCGDCGWLARRGLAEHHAHLAPPEL 	
hUOG-1	MAAAGPAAGPTGPEPMP SYAQLVQRGWGSALAAARGCTDCGWLARRGLAEHHAHLAPPEL 	60
	1	
	61	120
mUOG-1	LLAVLCALGWTALRWAATTHIFRPLAKRCRLQPRDAARLPESAWKLLFYLCWSYCA YLL 	
hUOG-1	LLALGALGWTALRSAATARLFRPLAKRCCLQPRDAAKMPESAWKLFYLGWSYSAYLL 	120
	61	180
	121	
mUOG-1	LGTSYPFFHDPPSVFYDWRSGMAVPWDIAVAYLLQGSFYCHSIYATVYMDSWRKDSVVM L 	
hUOG-1	FGTDYPFFHDPPSVFYDWTGMAVPRDIAAAYLLQGSFYGHSIYATLYMDTWRKDSVVM L 	180
	121	

FIG. 13b

mUOG-1	181	VHHVVTLLLIASSYAFRYHNVGGLLVFFLHVDVSDVQLEFTKLNIFYKARGGAYHRLHGLVA	240
hUOG-1	181	LHHVVTLLILIVSSYAFRYHNVGILVLFHLDISDVQLEFTKLNIFYKSRGGSYHRLHALAA	240
mUOG-1	241	NLGCLSF CFCWFWRLYWFLKVLVYATCHCSLQSVDPDIPYFFFNILLLLMVMNIYWFL	300
hUOG-1	241	DLGCLSEGF SFWWRLYWFLKVLVYATSHCSLRTVPDIPYFFFNALLLLTLMNLYWFL	300
mUOG-1	301	YIVAF AAKVLTGQMRELEDLREYDTLEAQTAKPCKAEKPLRNGLVKDKLF	350
hUOG-1	301	YIVAF AAKVLTGQVHELKDLREYDTAEASLKP SAEKPLRNGLVKDKRF	350

FIG. 13b cont.'

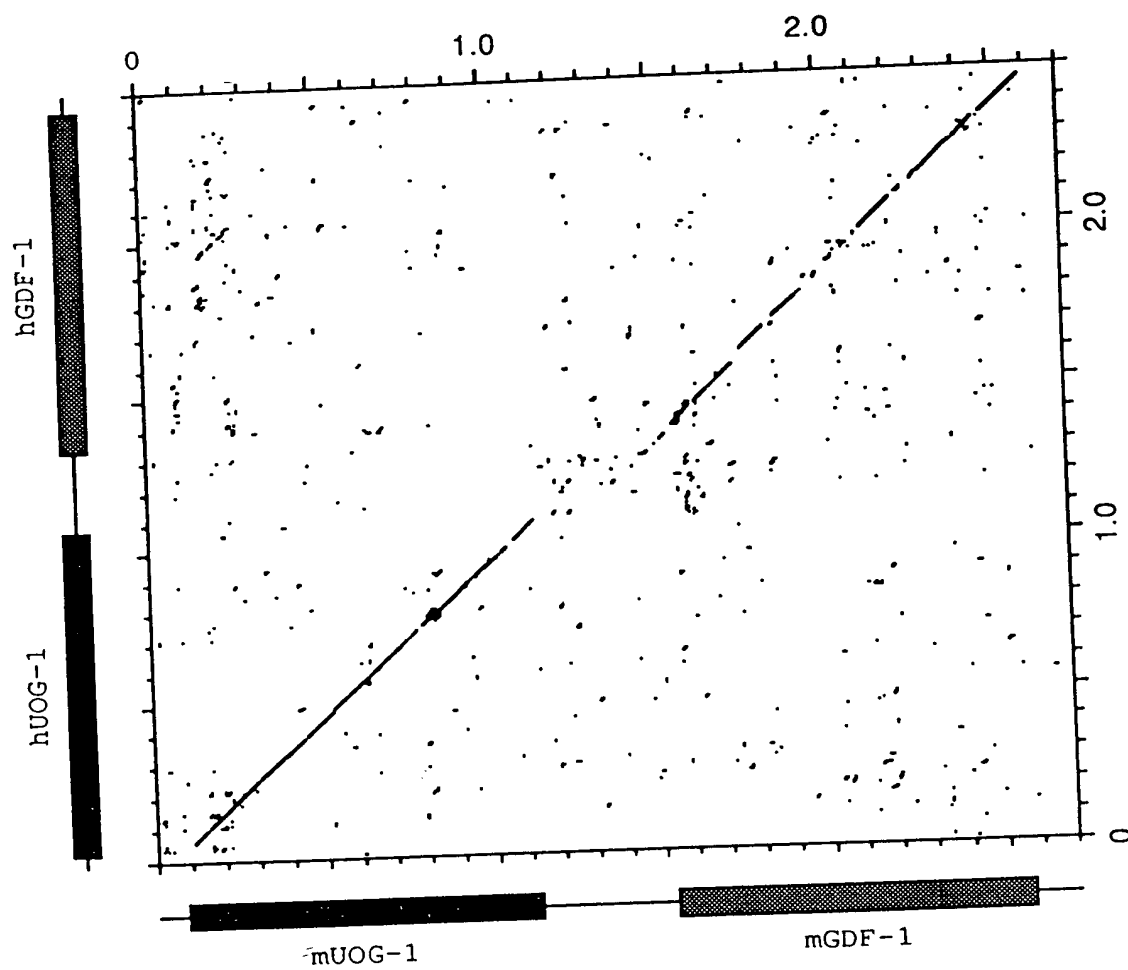


FIG. 13c

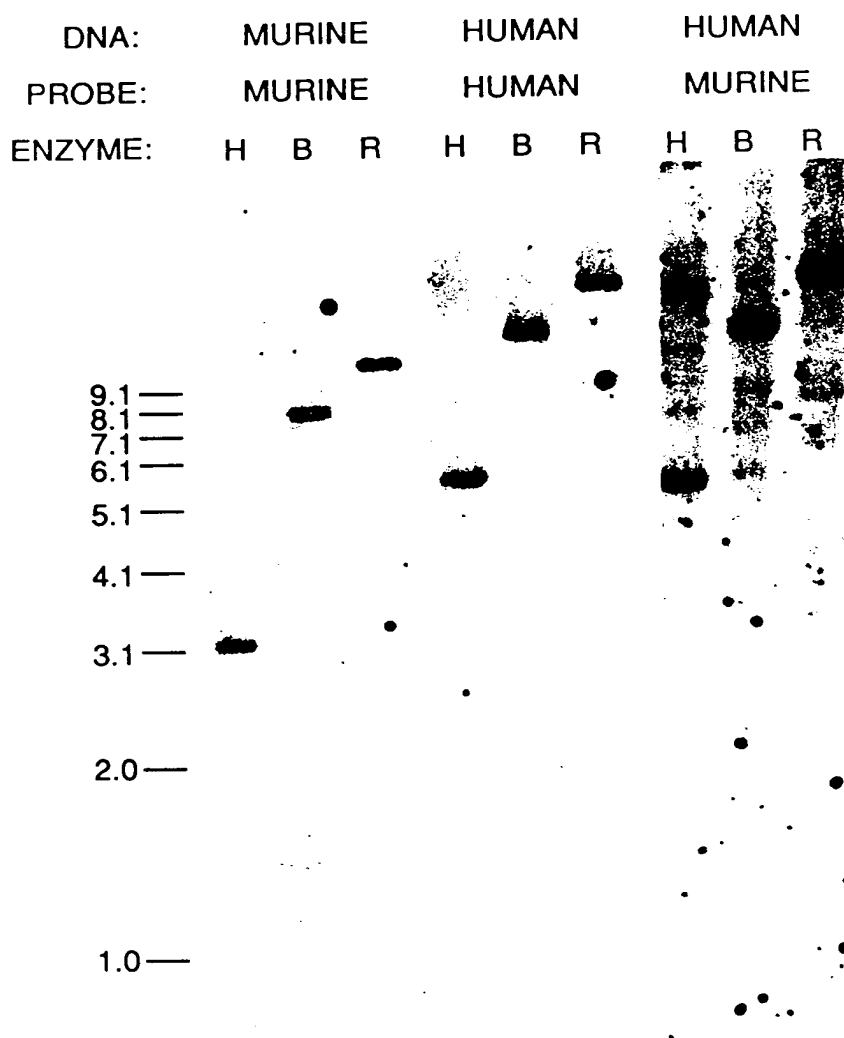


FIG. 14